

RAW SEQUENCE LISTING
ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/941947
Source: OIPE
Date Processed by STIC: 09/18/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>



Raw Sequence Listing Error Summary

ERROR DETECTED

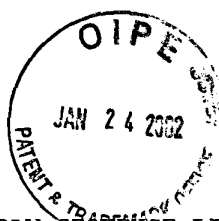
SUGGESTED CORRECTION

SERIAL NUMBER: 09/941947

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO

- 1 Wrapped Nucleics
 Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length
Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(ii) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
 (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents
- 10 Invalid <213>
 Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☒ Use of <220>
Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



OIPE

RAW SEQUENCE LISTING

DATE: 09/18/2001

PATENT APPLICATION: US/09/941,947

TIME: 10:40:16

Input Set : A:\CL1903 US NA Seq Listing.txt

Output Set: N:\CRF3\09182001\I941947.raw

Does Not Comply
Corrected Diskette Needed

See Page 6 of 7A

```

5 <110> APPLICANT: Brzostowicz, Patricia C.
6      Cheng, Qiong
7      DiCosimo, Deana J.
8      Koffas, Mattheos
9      Miller, Edward S. Jr.
10     Odom, J. Martin
11     Picataggio, Steve
12     Rouviere, Pierre E.
16 <120> TITLE OF INVENTION: CAROTENOID PRODUCTION FROM A SINGLE CARBON SOURCE
20 <130> FILE REFERENCE: CL1903 US NA
C--> 23 <140> CURRENT APPLICATION NUMBER: US/09/941,947
C--> 23 <141> CURRENT FILING DATE: 2001-08-29
23 <150> PRIOR APPLICATION NUMBER: 60/229,907
24 <151> PRIOR FILING DATE: 2000-09-01
26 <150> PRIOR APPLICATION NUMBER: 60/229,858
27 <151> PRIOR FILING DATE: 2000-09-01
29 <160> NUMBER OF SEQ ID NOS: 60
33 <170> SOFTWARE: Microsoft Office 97
37 <210> SEQ ID NO: 1
39 <211> LENGTH: 1311
41 <212> TYPE: DNA
43 <213> ORGANISM: Methylobacterium 16a
47 <400> SEQUENCE: 1
48 gatgtggtca catggcccta tcaactaacg gctgatattc gattttgtca ttggtttttt 60
50 cttaaacttta acttctacac gctcatgaac aaacctaaaa aagttgcaat actgacagca 120
52 ggcggcttgg cgccttgttt gaattccgca atcggtagtt tgatcgaacg ttataccgaa 180
54 atcgatccta gcatagaaat catttgctat cgcggcggtt ataaaggcct gttgctgggc 240
56 gattcttatc cagtaacggc cgaagtgcgt aaaaaggcgg gtgttctgca acgttttggc 300
58 ggttctgtga tcggcaacag cgcgcgtcaa ttgaccaatg tcaaagactg cgtgaaacgc 360
60 ggttttgtca aagaggggtga agatccgcaa aaagtccggc ctgatcaatt ggttaaggat 420
62 ggtgtcgata ttctgcacac catcggcggc gatgatacca atacggcagc agcggatttg 480
64 gcagcattcc tggccagaaa taattacgga ctgaccgtca ttggtttacc taaaaccgtc 540
66 gataacgacg tatttccgat caagcaatca ctagggtgct ggactgccgc cgagcaaggc 600
68 gcgcgttatt tcatgaacgt ggtggccgaa aacaacgcca acccagcat gctgatcgta 660
70 cacgaagtga tgggccgtaa ctgcggctgg ctgaccgtg caaccgcgca ggaatatcgc 720
72 aaattactgg accgtgccga gtggttgccg gaattgggtt tgactcgtga atcttatgaa 780
74 gtgcacgcgg tattcgttcc ggaaatggcg atcgacctg aagccgaagc caagcgctg 840
76 cgcgaagtga tggacaaagt cgattgcgtc aacatcttcg ttccgaagg tgccggcgtc 900
78 gaagctatcg tcgcggaat gcaggccaaa ggccaggaag tgccgcgcga tgcgttcggc 960
80 cacatcaaac tggatgcggt caaccctggt aaatggttcg gcgagcaatt cgcgcagatg 1020
82 ataggcgcg aaaaaaccct ggtacaaaaa tcgggatact tcgccgtgc ttctgcttcc 1080
84 aacgttgacg acatgcgttt gatcaaatcg tgcgccgact tggcggtcga gtgcgcgttc 1140
86 cgcgcgagat ctggcgtgat cggtcacgac gaagacaacg gcaacgtgtt gcgtgcgatc 1200
88 gagtttccgc gcatcaaggg cggcaaaccg ttcaatatcg acaccgactg gttcaatagc 1260
90 atgttgagcg aaatcggcca gcctaaaggc ggtaaagtcg aagtcagcca c 1311
93 <210> SEQ ID NO: 2
95 <211> LENGTH: 437

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RAW SEQUENCE LISTING

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Input Set : A:\CL1903 US NA Seq Listing.txt

Output Set: N:\CRF3\09182001\I941947.raw

97 <212> TYPE: PRT

99 <213> ORGANISM: Methylomonas 16a

103 <400> SEQUENCE: 2

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105 Asp Val Val Thr Trp Pro Tyr His Leu Thr Ala Asp Ile Arg Phe Cys
106 1 5 10 15
109 His Trp Phe Phe Leu Asn Phe Asn Phe Tyr Thr Leu Met Asn Lys Pro
110 20 25 30
113 Lys Lys Val Ala Ile Leu Thr Ala Gly Gly Leu Ala Pro Cys Leu Asn
114 35 40 45
117 Ser Ala Ile Gly Ser Leu Ile Glu Arg Tyr Thr Glu Ile Asp Pro Ser
118 50 55 60
121 Ile Glu Ile Ile Cys Tyr Arg Gly Gly Tyr Lys Gly Leu Leu Leu Gly
122 65 70 75 80
125 Asp Ser Tyr Pro Val Thr Ala Glu Val Arg Lys Lys Ala Gly Val Leu
126 85 90 95
129 Gln Arg Phe Gly Gly Ser Val Ile Gly Asn Ser Arg Val Lys Leu Thr
130 100 105 110
133 Asn Val Lys Asp Cys Val Lys Arg Gly Leu Val Lys Glu Gly Glu Asp
134 115 120 125
137 Pro Gln Lys Val Ala Ala Asp Gln Leu Val Lys Asp Gly Val Asp Ile
138 130 135 140
141 Leu His Thr Ile Gly Gly Asp Asp Thr Asn Thr Ala Ala Ala Asp Leu
142 145 150 155 160
145 Ala Ala Phe Leu Ala Arg Asn Asn Tyr Gly Leu Thr Val Ile Gly Leu
146 165 170 175
149 Pro Lys Thr Val Asp Asn Asp Val Phe Pro Ile Lys Gln Ser Leu Gly
150 180 185 190
153 Ala Trp Thr Ala Ala Glu Gln Gly Ala Arg Tyr Phe Met Asn Val Val
154 195 200 205
157 Ala Glu Asn Asn Ala Asn Pro Arg Met Leu Ile Val His Glu Val Met
158 210 215 220
161 Gly Arg Asn Cys Gly Trp Leu Thr Ala Ala Thr Ala Gln Glu Tyr Arg
162 225 230 235 240
165 Lys Leu Leu Asp Arg Ala Glu Trp Leu Pro Glu Leu Gly Leu Thr Arg
166 245 250 255
169 Glu Ser Tyr Glu Val His Ala Val Phe Val Pro Glu Met Ala Ile Asp
170 260 265 270
173 Leu Glu Ala Glu Ala Lys Arg Leu Arg Glu Val Met Asp Lys Val Asp
174 275 280 285
177 Cys Val Asn Ile Phe Val Ser Glu Gly Ala Gly Val Glu Ala Ile Val
178 290 295 300
181 Ala Glu Met Gln Ala Lys Gly Gln Glu Val Pro Arg Asp Ala Phe Gly
182 305 310 315 320
185 His Ile Lys Leu Asp Ala Val Asn Pro Gly Lys Trp Phe Gly Glu Gln
186 325 330 335
189 Phe Ala Gln Met Ile Gly Ala Glu Lys Thr Leu Val Gln Lys Ser Gly
190 340 345 350
193 Tyr Phe Ala Arg Ala Ser Ala Ser Asn Val Asp Asp Met Arg Leu Ile
194 355 360 365

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Input Set : A:\CL1903 US NA Seq Listing.txt

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197 Lys Ser Cys Ala Asp Leu Ala Val Glu Cys Ala Phe Arg Arg Glu Ser
198      370                      375                      380
201 Gly Val Ile Gly His Asp Glu Asp Asn Gly Asn Val Leu Arg Ala Ile
202 385                      390                      395                      400
205 Glu Phe Pro Arg Ile Lys Gly Gly Lys Pro Phe Asn Ile Asp Thr Asp
206                      405                      410                      415
209 Trp Phe Asn Ser Met Leu Ser Glu Ile Gly Gln Pro Lys Gly Gly Lys
210                      420                      425                      430
213 Val Glu Val Ser His
214      435
217 <210> SEQ ID NO: 3
219 <211> LENGTH: 636
221 <212> TYPE: DNA
223 <213> ORGANISM: Methylomonas 16a
227 <400> SEQUENCE: 3
228 gaaaataacta tgtccgtcac catcaaagaa gtcatgacca cctcgcccggt tatgccgggtc      60
230 atggtcatca atcatctgga acatgccgtc cctctgggtc gcgcgctagt cgacgggtggc      120
232 ttgaaagttt tggagatcac attgcgcacg ccggtggcac tggaatgtat ccgacgtatc      180
234 aaagccgaag taccggacgc catcgtcggc gcgggcacca tcatcaaccc tcataccttg      240
236 tatcaagcga ttgacgccgg tgcggaattc atcgtcagcc ccggcatcac cgaaaatcta      300
238 ctcaacgaag cgctagcatc cggcgtgcct atcctgcccg gcgtcatcac acccagcgag      360
240 gtcatgcgtt tattggaaaa aggcatcaat gcgatgaaat tctttccggc tgaagccgcc      420
242 ggcggcatac cgatgctgaa atcccttggc ggccccttgc cgcaagtcac cttctgtccg      480
244 accggcgggc tcaatcccaa aaacgcgccc gaatatctgg cattgaaaaa tgtcgctgc      540
246 gtcggcggtt cctggatggc gccggccgat ctggtagatg ccgaagactg ggcggaaatc      600
248 acgcggcggg cgagcgaggc cgcggcattg aaaaaa      636
251 <210> SEQ ID NO: 4
253 <211> LENGTH: 212
255 <212> TYPE: PRT
257 <213> ORGANISM: Methylomonas 16a
261 <400> SEQUENCE: 4
263 Glu Asn Thr Met Ser Val Thr Ile Lys Glu Val Met Thr Thr Ser Pro
264 1      5      10      15
267 Val Met Pro Val Met Val Ile Asn His Leu Glu His Ala Val Pro Leu
268      20      25      30
271 Ala Arg Ala Leu Val Asp Gly Gly Leu Lys Val Leu Glu Ile Thr Leu
272      35      40      45
275 Arg Thr Pro Val Ala Leu Glu Cys Ile Arg Arg Ile Lys Ala Glu Val
276      50      55      60
279 Pro Asp Ala Ile Val Gly Ala Gly Thr Ile Ile Asn Pro His Thr Leu
280 65      70      75      80
283 Tyr Gln Ala Ile Asp Ala Gly Ala Glu Phe Ile Val Ser Pro Gly Ile
284      85      90      95
287 Thr Glu Asn Leu Leu Asn Glu Ala Leu Ala Ser Gly Val Pro Ile Leu
288      100      105      110
291 Pro Gly Val Ile Thr Pro Ser Glu Val Met Arg Leu Leu Glu Lys Gly
292      115      120      125
295 Ile Asn Ala Met Lys Phe Phe Pro Ala Glu Ala Ala Gly Gly Ile Pro
296      130      135      140

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Input Set : A:\CL1903 US NA Seq Listing.txt

Output Set: N:\CRF3\09182001\I941947.raw

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299 Met Leu Lys Ser Leu Gly Gly Pro Leu Pro Gln Val Thr Phe Cys Pro
300 145                      150                      155                      160
303 Thr Gly Gly Val Asn Pro Lys Asn Ala Pro Glu Tyr Leu Ala Leu Lys
304                      165                      170                      175
307 Asn Val Ala Cys Val Gly Gly Ser Trp Met Ala Pro Ala Asp Leu Val
308                      180                      185                      190
311 Asp Ala Glu Asp Trp Ala Glu Ile Thr Arg Arg Ala Ser Glu Ala Ala
312                      195                      200                      205
315 Ala Leu Lys Lys
316                      210
319 <210> SEQ ID NO: 5
321 <211> LENGTH: 1860
323 <212> TYPE: DNA
325 <213> ORGANISM: Methylobacterium 16a
329 <400> SEQUENCE: 5
330 atgaactga ccaccgacta tcccttgctt aaaaacatcc acacgccggc ggacatacgc      60
332 gcgctgtcca aggaccagct ccagcaactg gctgacgagg tgcgcggcta tctgaccac      120
334 acggtcagca ttccggcg ccattttgcg gccggcctcg gcaccgtgga actgaccgtg      180
336 gccttgcat atgtgttcaa taccctcgtc gatcagttgg tctgggacgt gggccatcag      240
338 gcctatccgc acaagattct gaccggtcgc aaggagcgca tgccgacat tcgcacctg      300
340 ggcggggtgt cagcctttcc ggcgcgggac gagagcgaat acgatgcctt cggcgctcggc      360
342 cattccagca cctcgatcag cgcggcactg ggcatggcca ttgcgtcgca gctgcgcggc      420
344 gaagacaaga agatggtagc catcatcggc gacggttcca tcaccggcg catggcctat      480
346 gaggcgatga atcatgcgg cgatgtgaat gccaacctgc tggatgattt gaacgacaac      540
348 gatattgtga tctcgccg ccggtcgggc atgaacaatt atctgacca ggtgtgtgtc      600
350 agcaagtttt attcgctcgg gcgggaagag agcaagaaag ctctggccaa gatgccgtcg      660
352 gtgtgggaac tggcgcgcaa gaccgaggaa cagctgaagg gcatgatcgt gcccggtacc      720
354 ttgttcgagg aattgggctt caattatttc ggcccgatcg acggccatga tgtcgagatg      780
356 ctggtgtcga ccctggaaaa tctgaaggat ttgaccgggc cgttattcct gcatgtgtgt      840
358 accaagaagg gcaaaggcta tgcgccagcc gagaaagacc cgttggccta ccatggcgtg      900
360 ccggctttcg atcgaccaa ggatttcctg cccaaggcgg cgcgctcgcc gcatccgacc      960
362 tataccgagg tgttcggccg ctggctgtgc gacatggcgg ctcaagacga gcgcttgctg      1020
364 ggcatcacgc cggcgatcgc cgaaggctct ggtttggttg aattctcaca gaaatttccg      1080
366 aatcgctatt tcgatgtcgc catcgccgag cagcatgcgg tgacctggc cgcggccag      1140
368 gcctgccagg gcgccaagcc ggtggtggcg atttattcca ccttcctgca acgcggttac      1200
370 gatcagttga tccacgacgt ggccttgtag aacttagata tgctctttgc actggatcgt      1260
372 gccggcttgg tcggcccgga tggaccgacc catgctggcg cctttgatta cagctacatg      1320
374 cgctgtattc cgaacatgct gatcatggtt ccagccgacg agaacgagtg caggcagatg      1380
376 ctgaccaccg gcttccaaca ccatggcccg gcttcggtgc gctatccgcg cggcaaaggg      1440
378 ccggggcgcg caatcgatcc gaccctgacc gcgctggaga tcggcaaggc cgaagtcaga      1500
380 caccacggca gccgcacgc cattctggcc tggggcagca tggtcacgcc tgccgtcgaa      1560
382 gccggcaagc agctgggcgc gacggtggtg aacatgcgtt tcgtcaagcc gttcgatcaa      1620
384 gccttggtgc tggaaattgg caggacgcac gatgtgttcg tcaccgtcga gaaaaacgtc      1680
386 atcgccggcg gcgctggcag tgcgatcaac accttcctgc aggcgcagaa ggtgctgatg      1740
388 ccggtctgca acatcgccct gcccgaccgc ttcgctcagc aaggtagtcg cgaggaattg      1800
390 ctacgcttgg tcggcctcga cagcaaggcc atcctcgcca ccatcgaaca gttttgcgct      1860
393 <210> SEQ ID NO: 6
395 <211> LENGTH: 620
397 <212> TYPE: PRT

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<210> SEQ ID NO 41
<211> LENGTH: 38
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION:
<400> SEQUENCE: 41
agcagctagc ggaggaataa accatgagcg catttoto
38

Errored

<210> SEQ ID NO 42
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: :
<400> SEQUENCE: 42
gactagtcac gacctgctcg aacgac
26

Errored

Errored: When the ORGANISM field is "Artificial Sequence"
an explanation is mandatory in field 223.

The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/941,947

DATE: 09/18/2001

TIME: 10:40:17

Input Set : A:\CL1903 US NA Seq Listing.txt

Output Set: N:\CRF3\09182001\I941947.raw

L:23 M:270 C: Current Application Number differs, Replaced Current Application No
L:23 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:3057 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:41
L:3061 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:3061 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:3071 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:42
L:3075 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:3075 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:

US 0994194707P1



Creation date: 28-08-2003
Indexing Officer: FPLUMMER - FRANCIS PLUMMER
Team: OIPEBackFileIndexing
Dossier: 09941947

Legal Date: 19-02-2002

| No. | Doccode | Number of pages |
|-----|---------|-----------------|
| 1 | CRFL | 8 |

Total number of pages: 8

Remarks:

Order of re-scan issued on